

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 10/612,468B
Source: 1FW/6
Date Processed by STIC: 1/10/07

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- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

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1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/612,468B

DATE: 01/10/2007
TIME: 09:43:35

Input Set : A:\D6622SEQ.txt
Output Set: N:\CRF4\0110200\J612468B.raw

3 <110> APPLICANT: Zhang, Jingwu Z.
4 Ho, Walter Kowk Keung
5 Zhang, Dongqing
6 Sun, Wei
8 <120> TITLE OF INVENTION: T Cell Receptor CDR3 Sequence and Methods for
9 Detecting and Treating Rheumatoid Arthritis
11 <130> FILE REFERENCE: D6622
13 <140> CURRENT APPLICATION NUMBER: US 10/612,468B
14 <141> CURRENT FILING DATE: 2003-07-02
16 <150> NUMBER OF SEQ ID NOS: 168

see pg 1-3

ERRORED SEQUENCES

416 <210> SEQ ID NO: 29
417 <211> LENGTH: 21
418 <212> TYPE: DNA
419 <213> ORGANISM: Artificial Sequence
421 <220> FEATURE:
422 <221> NAME/KEY: primer_bind
423 <223> OTHER INFORMATION: reverse primer specific for TCR BV11 used in real-time
424 PCR analysis *insert a hard return after <400729*
426 <400> SEQUENCE: 29 *atgtgaggc ctggcagact c* 21

688 <210> SEQ ID NO: 50
689 <211> LENGTH: 23
E--> 690 *225 DNA* <212>
691 <213> ORGANISM: Artificial Sequence
693 <220> FEATURE:
694 <221> NAME/KEY: primer_bind
695 <223> OTHER INFORMATION: forward primer specific for TCR BV22 used in real-time
696 PCR analysis

698 <400> SEQUENCE: 50
699 cacagatggg acaggaagtg atc 23
727 <210> SEQ ID NO: 53
728 <211> LENGTH: 21
729 <212> TYPE: DNA
730 <213> ORGANISM: Artificial Sequence
732 <220> FEATURE: <221>
E--> 733 <21> primer_bind <221>
734 <223> OTHER INFORMATION: reverse primer specific for TCR BV23 used in real-time PCR analysis

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING DATE: 01/10/2007
 PATENT APPLICATION: US/10/612,468B TIME: 09:43:35

Input Set : A:\D6622SEQ.txt
 Output Set: N:\CRF4\01102007\J612468B.raw

737 <400> SEQUENCE: 53
 738 cagctccaag gagctcatgt t 21
 740 <210> SEQ ID NO: 54
 741 <211> LENGTH: 24
 742 <212> TYPE: DNA
 743 <213> ORGANISM: Artificial Sequence
 745 <220> FEATURE:
 746 <221> NAME/KEY: primer_bind
 747 <223> OTHER INFORMATION: forward primer specific for TCR BV24 used in real-time PCR analysis *Insert a hard return*
 750 <400> SEQUENCE: 54 ccaagataacc aggttaccca gttt 24

1271 <210> SEQ ID NO: 93
 1272 <211> LENGTH: 20
 1273 <212> TYPE: PRT
 1274 <213> ORGANISM: Homo sapiens
 1276 <220> FEATURE:
 1277 <221> NAME/KEY: Domain
 1278 <223> OTHER INFORMATION: CDR3 amino acid sequence of BV16 clonotype derived from ST specimen of RA patient
 1281 <400> SEQUENCE: 93
 1282 Tyr Phe Cys Ala Ser Ser Gln Ala Asp Gly Thr His Tyr Glu Gln
 1283 5 10 15
 1284 Phe Phe Gly Pro Gly
 E--> 1285 ~~20~~ 20 *misaligned amino acid number*
 1287 <210> SEQ ID NO: 94
 1288 <211> LENGTH: 60 <2127
 E--> 1289 <213> DNA
 1290 <213> ORGANISM: Artificial Sequence
 1292 <220> FEATURE:
 1293 <221> NAME/KEY: CDS
 1294 <223> OTHER INFORMATION: CDR3 nucleic acid sequence of BV16 clonotype derived from ST specimen of RA patients
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 1298 <400> SEQUENCE: 94
 1299 tatttctgtg ccagcagcca agctgacggg acccattacg agcagtactt 50
 1300 cgggcccggc 60
 1968 <210> SEQ ID NO: 140
 1969 <211> LENGTH: 57 <2127
 E--> 1970 <213> DNA
 1971 <213> ORGANISM: Artificial Sequence
 1973 <220> FEATURE:
 1974 <221> NAME/KEY: CDS
 1975 <223> OTHER INFORMATION: CDR3 nucleic acid sequence of BV14 clonotype derived from ST specimen of RA patients
 1976
 1978 <400> SEQUENCE: 140
 1979 tacttctgtg ccagcagttt atcttcgaca gggagggagc agtacttcgg gccgggc 57
 2371 <210> SEQ ID NO: 168

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/612,468B

DATE: 01/10/2007

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Input Set : A:\D6622SEQ.txt

Output Set: N:\CRF4\01102007\J612468B.raw

2372 <211> LENGTH: 54
2373 <212> TYPE: DNA
2374 <213> ORGANISM: Artificial Sequence
2376 <220> FEATURE:
2377 <221> NAME/KEY: CDS
2378 <223> OTHER INFORMATION: CDR3 nucleic acid sequence of BV14 clonotype derived
from ST specimen of RA patients
2381 <400> SEQUENCE: 168
2382 tacttctgtg ccagcagttc cctcgctact gctgaagctt tctttggaca aggc 54
E--> 2383 ??
E--> 2385 ??
E--> 2387 ??
E--> 2389 ??

delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/612,468B

DATE: 01/10/2007

TIME: 09:43:36

Input Set : A:\D6622SEQ.txt

Output Set: N:\CRF4\01102007\J612468B.raw

L:426 M:301 E: (44) No Sequence Data was Shown, SEQ ID:29
L:426 M:252 E: No. of Seq. differs, <211> LENGTH:Input:21 Found:0 SEQ:29
L:690 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:698 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:733 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:750 M:301 E: (44) No Sequence Data was Shown, SEQ ID:54
L:750 M:252 E: No. of Seq. differs, <211> LENGTH:Input:24 Found:0 SEQ:54
L:1285 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:93
L:1289 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:1298 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:1970 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:1978 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:2383 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:168
L:2385 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:168
L:2387 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2389 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:168
L:2389 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1